Appendix 2 – Marked-up copies of amended paragraphs

Marked up amended paragraphs at p.15, line ~~25~~ 24 to p.16, line ~~14~~ 13. KW 4/5/07

Fig. 6 shows the tryptic peptide mass spectrum analysis of the PT72 protein interacting with 96 ORF 78. The gel slice containing PT72 contained one protein. The PT72 band was identified as an open reading frame, herein referred as STAAU_R9, found in Contig 286 of the University of Oklahoma genome sequencing project database ~~(http://www.genome.ou.edu/staph.html)~~ (Web site with the remainder of the address being genome.ou.edu/staph.html) (SEQ ID NOS 29-36).

Fig. 7 shows the results of amino acid sequence analysis of STAAU_R9. A) Results of the STAAU_R9 Hidden Markov Model (HMM) searching analysis of the publically available Pfam database identifying two conserved Pfam motifs: Zf-CHC2 (SEQ ID NO: 37) compared with STAAU_R9 (residues 3-100 of SEQ ID NO: 2) and Toprim (SEQ ID NO: 38) compared with STAAU_R9 (residues 260-339 of SEQ ID NO: 2). B) Results of the global optimal alignment of the amino acid sequences of different STAAU_R9-related sequences. STAAU_R9 (SEQ ID NO: 2) is highly similar to *S. aureus* DNA primase (SEQ ID NO: 39) (92% identity to gi|2494147|sp|O05338|PRIM_STAAU DNA PRIMASE, DnaG). Note the discrepancies between the sequences of DNA primase from *S. aureus* as reported in Swissprot and as predicted from the University of Oklahoma *S. aureus* genome sequencing project database. STAAU_R9 (SEQ ID NO: 2) is also moderately similar to a variety of bacterial DNA primase proteins including *B. stearothermophilus* DnaG (SEQ ID NO: 40) (34% identity to gi|9910841|sp|Q9X4D0|PRIM_BACST DNA PRIMASE) *B. subtilis* DnaG (SEQ ID NO: 41) (36% identity to gi|130904|sp|P05096|PRIM_BACSU DNA PRIMASE) and *E. coli* DnaG (SEQ ID NO: 22) (27% identity to gi|130908|sp|P02923|PRIM_ECOLI DNA PRIMASE).

Marked-up amended paragraph for p.17, lines 22-26.

Fig. 11 shows the list of the oligonucleotide primers (SEQ ID NOS 8-21 and 7, respectively in order of appearance) used for amplification by PCR and cloning of